

Supplemental Table 1. Cell lines analyzed in mutational screening.

| Cell Line Name | Tumor Type | Translocation |
|----------------|------------|-----------------|
| JN-DSRCT | DSRCT | EWS-WT1 |
| A4573 | EFT | EWS-FLI1 type 3 |
| A673 | EFT | EWS-FLI1 type 1 |
| RD-ES | EFT | EWS-FLI1 type 2 |
| SKES1 | EFT | EWS-FLI1 type 2 |
| SKPNDW | EFT | EWS-FLI1 type 1 |
| TC32 | EFT | EWS-FLI1 type 1 |
| TC71 | EFT | EWS-FLI1 type 1 |
| Cado-ES | EFT | EWS-ERG |
| 6647 | EFT | EWS-FLI1 type 2 |
| MHH-ES-1 | EFT | EWS-FLI1 type 2 |
| RMS559 | ERMS | Negative |
| RD | ERMS | Negative |
| SMS-CTR | ERMS | Negative |
| RH18C | ARMS | Negative |
| CW9019 | ARMS | PAX7-FKHR |
| SCMC-RM2 | ARMS | PAX3-FKHR |
| RH28 | ARMS | PAX3-FKHR |
| RH30 | ARMS | PAX3-FKHR |
| TS-RM1 | ARMS | PAX3-FKHR |
| JR | ARMS | PAX3-FKHR |
| RH-41 | ARMS | PAX3-FKHR |

Supplemental Table 2. Point mutations across all 29 interrogated genes listed in table 1.

| Gene | Amino Acid | Nucleotide |
|------|------------|----------------|
| AKT1 | p.E17K | c.49G>A |
| AKT2 | p.E17K | c.49G>A |
| AKT3 | p.E17K | c.49G>A |
| ALK | p.K1062M | c.3184A>T |
| ALK | p.D1091N | c.3271G>A |
| ALK | p.M1166R | c.3497T>G |
| ALK | p.I1171N | c.3512T>A |
| ALK | p.F1174I | c.3520aTTC>A |
| ALK | p.F1174L | c.3520aTTC>C |
| ALK | p.F1174V | c.3520aTTC>GTC |
| ALK | p.F1174C | c.3521T>G |
| ALK | p.F1174L | c.3522C>A |
| ALK | p.A1234T | c.3700G>A |
| ALK | p.F1245V | c.3733T>G |
| ALK | p.F1245C | c.3734T>G |
| ALK | p.F1245L | c.3735C>A |
| ALK | p.F1245L | c.3735C>G |
| ALK | p.I1250T | c.3749T>C |
| ALK | p.R1275Q | c.3824G>A |
| ALK | p.Y1278S | c.3832A>C |
| BRAF | p.G464R | c.1390G>C |
| BRAF | p.G464E | c.1391G>A |
| BRAF | p.G464V | c.1391G>T |
| BRAF | p.S467A | c.1399T>G |
| BRAF | p.F468S | c.1403T>C |
| BRAF | p.F468C | c.1403T>G |
| BRAF | p.G469E | c.1406G>A |
| BRAF | p.G469A | c.1406G>C |
| BRAF | p.G469V | c.1406G>T |
| BRAF | p.L485F | c.1455G>C |
| BRAF | p.V487G | c.1460T>G |
| BRAF | p.K499E | c.1495A>G |
| BRAF | p.K499N | c.1497A>C |
| BRAF | p.E501K | c.1501G>A |
| BRAF | p.E501G | c.1502A>G |
| BRAF | p.E501V | c.1502A>T |
| BRAF | p.N580D | c.1738A>G |
| BRAF | p.N581D | c.1741A>G |
| BRAF | p.N581S | c.1742A>G |
| BRAF | p.N581I | c.1742A>T |

| | | |
|--------|---------|-----------|
| BRAF | p.N581K | c.1743T>A |
| BRAF | p.D594G | c.1781A>G |
| BRAF | p.D594V | c.1781A>T |
| BRAF | p.F595L | c.1783T>C |
| BRAF | p.F595S | c.1784T>C |
| BRAF | p.F595L | c.1785T>A |
| BRAF | p.F595L | c.1785T>G |
| BRAF | p.G596R | c.1786G>C |
| BRAF | p.G596D | c.1787G>A |
| BRAF | p.G596V | c.1787G>T |
| BRAF | p.V600M | c.1798G>A |
| BRAF | p.V600E | c.1799T>A |
| BRAF | p.V600A | c.1799T>C |
| BRAF | p.V600G | c.1799T>G |
| BRAF | p.T241P | c.721A>C |
| BRAF | p.T244P | c.730A>C |
| BRAF | p.A246P | c.736G>C |
| BRAF | p.Q257K | c.769C>A |
| BRAF | p.Q257R | c.770A>G |
| BRAF | p.Q262K | c.784C>A |
| BRAF | p.Q262R | c.785A>G |
| CDK4 | p.R24C | c.70C>T |
| CDK4 | p.R24L | c.71G>T |
| CTNNB1 | p.G34E | c.101G>A |
| CTNNB1 | p.G34V | c.101G>T |
| CTNNB1 | p.S37T | c.109T>A |
| CTNNB1 | p.S37P | c.109T>C |
| CTNNB1 | p.S37A | c.109T>G |
| CTNNB1 | p.T41P | c.121A>C |
| CTNNB1 | p.T41A | c.121A>G |
| CTNNB1 | p.T41S | c.121A>T |
| CTNNB1 | p.T41N | c.122C>A |
| CTNNB1 | p.T41S | c.122C>G |
| CTNNB1 | p.T41I | c.122C>T |
| CTNNB1 | p.S45T | c.133T>A |
| CTNNB1 | p.S45P | c.133T>C |
| CTNNB1 | p.S45A | c.133T>G |
| CTNNB1 | p.S45Y | c.134C>A |
| CTNNB1 | p.S45C | c.134C>G |
| CTNNB1 | p.S45F | c.134C>T |
| CTNNB1 | p.D32A | c.95A>C |

| | | |
|--------|---------|--------------------|
| CTNNB1 | p.D32G | c.95A>G |
| CTNNB1 | p.D32V | c.95A>T |
| EGFR | p.E709H | c.2125_2127GAA>CAT |
| EGFR | p.E709K | c.2125G>A |
| EGFR | p.E709A | c.2126A>C |
| EGFR | p.E709G | c.2126A>G |
| EGFR | p.E709V | c.2126A>T |
| EGFR | p.G719S | c.2155G>A |
| EGFR | p.G719C | c.2155G>T |
| EGFR | p.G719D | c.2156G>A |
| EGFR | p.G719A | c.2156G>C |
| EGFR | p.D761N | c.2281G>A |
| EGFR | p.D761Y | c.2281G>T |
| EGFR | p.S768I | c.2303G>T |
| EGFR | p.R776C | c.2326C>T |
| EGFR | p.R776H | c.2327G>A |
| EGFR | p.T790M | c.2369C>T |
| EGFR | p.T854A | c.2560A>G |
| EGFR | p.L858M | c.2572C>A |
| EGFR | p.L858R | c.2573T>G |
| EGFR | p.L861Q | c.2582T>A |
| EGFR | p.L861R | c.2582T>G |
| ERBB2 | p.V777L | c.2329G>T |
| ERBB2 | p.L755S | c.2264T>C |
| ERBB2 | p.D769H | c.2305G>C |
| ERBB2 | p.V777M | c.2329G>A |
| FGFR2 | p.N550K | c.1650T>A |
| FGFR2 | p.N550K | c.1650T>G |
| FGFR2 | p.S252W | c.755C>G |
| FGFR3 | p.G370C | c.1108G>T |
| FGFR3 | p.Y373C | c.1118A>G |
| FGFR3 | p.K650Q | c.1948aA>C |
| FGFR3 | p.K650E | c.1948aA>G |
| FGFR3 | p.K650T | c.1949A>C |
| FGFR3 | p.K650M | c.1949A>T |
| FGFR3 | p.G697C | c.2089G>T |
| FGFR3 | p.R248C | c.742C>T |
| FGFR3 | p.S249C | c.746C>G |
| FLT3 | p.D835N | c.2503G>A |
| FLT3 | p.D835H | c.2503G>C |
| FLT3 | p.D835Y | c.2503G>T |

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|------|---------|-----------|
| GNAQ | p.Q209L | c.626A>C |
| GNAQ | p.Q209P | c.626A>T |
| GNAQ | p.Q209H | c.627A>T |
| HRAS | p.Q61K | c.181C>A |
| HRAS | p.Q61E | c.181C>G |
| HRAS | p.Q61P | c.182A>C |
| HRAS | p.Q61R | c.182A>G |
| HRAS | p.Q61L | c.182A>T |
| HRAS | p.Q61H | c.183G>C |
| HRAS | p.Q61H | c.183G>T |
| HRAS | p.G12S | c.34G>A |
| HRAS | p.G12R | c.34G>C |
| HRAS | p.G12C | c.34G>T |
| HRAS | p.G12D | c.35G>A |
| HRAS | p.G12A | c.35G>C |
| HRAS | p.G12V | c.35G>T |
| HRAS | p.G13S | c.37G>A |
| HRAS | p.G13R | c.37G>C |
| HRAS | p.G13C | c.37G>T |
| HRAS | p.G13D | c.38G>A |
| HRAS | p.G13V | c.38G>T |
| IDH1 | p.R132S | c.394C>A |
| IDH1 | p.R132G | c.394C>G |
| IDH1 | p.R132C | c.394C>T |
| IDH1 | p.R132H | c.395aG>A |
| IDH1 | p.R132L | c.395bG>T |
| IDH2 | p.R172G | c.514A>G |
| IDH2 | p.R172K | c.515G>A |
| IDH2 | p.R172M | c.515G>T |
| JAK2 | p.V617F | c.1849G>T |
| KIT | p.V559D | c.1676T>A |
| KIT | p.V559A | c.1676T>C |
| KIT | p.V559G | c.1676T>G |
| KIT | p.D816V | c.2446G>A |
| KIT | p.D816H | c.2446G>C |
| KIT | p.D816A | c.2447A>C |
| KIT | p.D816G | c.2447A>G |
| KIT | p.D816V | c.2447A>T |
| KRAS | p.Q61K | c.181C>A |
| KRAS | p.Q61E | c.181C>G |
| KRAS | p.Q61P | c.182A>C |

| | | |
|--------|----------|----------------|
| KRAS | p.Q61R | c.182A>G |
| KRAS | p.Q61L | c.182A>T |
| KRAS | p.Q61H | c.183A>C |
| KRAS | p.Q61H | c.183A>T |
| KRAS | p.G12S | c.34G>A |
| KRAS | p.G12R | c.34G>C |
| KRAS | p.G12C | c.34G>T |
| KRAS | p.G12D | c.35G>A |
| KRAS | p.G12A | c.35G>C |
| KRAS | p.G12V | c.35G>T |
| KRAS | p.G13S | c.37G>A |
| KRAS | P.G13R | c.37G>C |
| KRAS | p.G13C | c.37G>T |
| KRAS | p.G13D | c.38G>A |
| KRAS | p.G13A | c.38G>C |
| KRAS | p.G13V | c.38G>T |
| KRAS | p.A146T | c.436G>A |
| KRAS | p.A146P | c.436G>C |
| KRAS | p.A146V | c.437C>T |
| KRAS | p.Q61K | c180_181 TC>CA |
| KRAS | p.K117N | c351A>C |
| KRAS | p.K117N | c351A>T |
| MAP2K1 | p.Q56P | c.167A>C |
| MAP2K1 | p.K57N | c.171G>T |
| MAP2K1 | p.D67N | c.199G>A |
| MET | p.Y1248C | c.3743A>G |
| MET | p.Y1253D | c.3757T>G |
| MET | p.M1268T | c.3803T>C |
| NOTCH1 | p.L1575P | c.4724T>C |
| NOTCH1 | p.L1586P | c.4757T>C |
| NOTCH1 | p.L1594P | c.4781T>C |
| NOTCH1 | p.R1599P | c.4796G>C |
| NOTCH1 | p.L1601P | c.4802T>C |
| NOTCH1 | p.L1679Q | c.5036T>A |
| NOTCH1 | p.L1679P | c.5036T>C |
| NOTCH1 | p.Q2460 | c.7378C>T |
| NRAS | p.Q61K | c.181C>A |
| NRAS | p.Q61K | c.181C>A |
| NRAS | p.Q61E | c.181C>G |
| NRAS | p.Q61E | c.181C>G |
| NRAS | p.Q61P | c.182A>C |

| | | |
|--------|---------|-----------|
| NRAS | p.Q61P | c.182A>C |
| NRAS | p.Q61R | c.182A>G |
| NRAS | p.Q61R | c.182A>G |
| NRAS | p.Q61L | c.182A>T |
| NRAS | p.Q61L | c.182A>T |
| NRAS | p.Q61H | c.183A>C |
| NRAS | p.Q61H | c.183A>C |
| NRAS | p.Q61Q | c.183A>G |
| NRAS | p.Q61H | c.183A>T |
| NRAS | p.Q61H | c.183A>T |
| NRAS | p.G12S | c.34G>A |
| NRAS | p.G12S | c.34G>A |
| NRAS | p.G12R | c.34G>C |
| NRAS | p.G12R | c.34G>C |
| NRAS | p.G12C | c.34G>T |
| NRAS | p.G12C | c.34G>T |
| NRAS | p.G12D | c.35G>A |
| NRAS | p.G12D | c.35G>A |
| NRAS | p.G12A | c.35G>C |
| NRAS | p.G12A | c.35G>C |
| NRAS | p.G12V | c.35G>T |
| NRAS | p.G12V | c.35G>T |
| NRAS | p.G13S | c.37G>A |
| NRAS | p.G13S | c.37G>A |
| NRAS | p.G13R | c.37G>C |
| NRAS | p.G13R | c.37G>C |
| NRAS | p.G13C | c.37G>T |
| NRAS | p.G13C | c.37G>T |
| NRAS | p.G13D | c.38G>A |
| NRAS | p.G13D | c.38G>A |
| NRAS | p.G13A | c.38G>C |
| NRAS | p.G13A | c.38G>C |
| NRAS | p.G13V | c.38G>T |
| NRAS | p.G13V | c.38G>T |
| PDGFRA | p.V561D | c.1682T>A |
| PDGFRA | p.D842V | c.2525A>T |
| PIK3CA | p.N345K | c.1035T>A |
| PIK3CA | p.N345K | c.1035T>G |
| PIK3CA | p.C420R | c.1258T>C |
| PIK3CA | p.E542K | c.1624G>A |
| PIK3CA | p.E542Q | c.1624G>C |

| | | |
|--------|----------|-----------|
| PIK3CA | p.E545K | c.1633G>A |
| PIK3CA | p.E545Q | c.1633G>C |
| PIK3CA | p.E545A | c.1634A>C |
| PIK3CA | p.E545G | c.1634A>G |
| PIK3CA | p.E545D | c.1635G>T |
| PIK3CA | p.R88Q | c.263G>A |
| PIK3CA | p.M1043I | c.3129G>T |
| PIK3CA | p.H1047Y | c.3139C>T |
| PIK3CA | p.H1047R | c.3140A>G |
| PIK3CA | p.H1047L | c.3140A>T |
| PIK3R1 | p.D560Y | c.1678G>T |
| PIK3R1 | p.N564K | c.1692C>A |
| PIK3R1 | p.N564K | c.1692C>G |
| PTPN11 | p.G60A | c.179G>C |
| PTPN11 | p.G60V | c.179G>T |
| PTPN11 | p.D61N | c.181G>A |
| PTPN11 | p.D61H | c.181G>C |
| PTPN11 | p.D61Y | c.181G>T |
| PTPN11 | p.D61G | c.182A>G |
| PTPN11 | p.D61V | c.182A>T |
| PTPN11 | p.A72T | c.214G>A |
| PTPN11 | p.E76K | c.226G>A |
| PTPN11 | p.E76Q | c.226G>C |
| PTPN11 | p.E76G | c.227A>G |
| PTPN11 | p.E76V | c.227A>T |
| PTPN11 | p.R152H | c.455G>A |
| RET | p.M918T | c.2753T>C |
| SMO | p.W535L | c.1604G>T |
| SMO | p.T640A | c.1918A>G |
| SMO | p.R199W | c.595C>T |

Supplemental table 3. List of primers used in Sequenom MassArray mutation detection assay.

| Assay Name | 1st Primer | 2nd Primer | UEP |
|------------|---------------------------------|---------------------------------|-----------------------------|
| AKT1_49G | ACGTTGGATGTAGAGTGTGCGTGGCTCTCA | ACGTTGGATGTTGAGGAGGAAGTAGCGTGG | CGCCAGGTCTTGATGTACT |
| AKT2_49 | ACGTTGGATGGTGGCCTCCAGGTCTTGAT | ACGTTGGATGCACTCAACCTTGCCTAACC | CTTCTGCCTCATTTTCAGGT |
| AKT3_49 | ACGTTGGATGAAAGGAAGTATCTTGGCCTC | ACGTTGGATGGCATTAAACATGCGTGCTTTC | tgccTGCCTGCTTTCTCATGTAGGA |
| ALK_3184 | ACGTTGGATGAGGCCATGTTGCAGCTGAC | ACGTTGGATGAGCTCCATCTGCATGGCTTG | agTGGCTTGAGCTCCTGGTGC |
| ALK_3271 | ACGTTGGATGTCTTGCCAGCAAAGCAGTAG | ACGTTGGATGCTGAGTACAAGCTGAGCAAG | CCTCGACCATCATGACC |
| ALK_3497 | ACGTTGGATGCTCTGTGGCTTTACCTGATG | ACGTTGGATGTGAAGTGTGCTCTGAACAGG | ctACGAACTGGATTTCTCA |
| ALK_3512 | ACGTTGGATGTGAGGGTGTCTCTCTGTGG | ACGTTGGATGAGTGTGCTCTGAACAGGACG | cgCATGGAAGCCCTGATCA |
| ALK_3520a | ACGTTGGATGATTGCAGGCTCACCCCAATG | ACGTTGGATGTTGGTTACATCCCTCTCTGC | TCTCTGCTCTGCAGCAA |
| ALK_3520b | ACGTTGGATGATTGCAGGCTCACCCCAATG | ACGTTGGATGTTGGTTACATCCCTCTCTGC | CTCTCTGCTCTGCAGCAAAT |
| ALK_3522 | ACGTTGGATGATTGCAGGCTCACCCCAATG | ACGTTGGATGTTGGTTACATCCCTCTCTGC | TCTCTGCTCTGCAGCAAAT |
| ALK_3700 | ACGTTGGATGCGGTGGATGAAGTGGTTTTTC | ACGTTGGATGATGCTGGACCTTCTGCACG | ccaaACGTGGCTCGGGACATT |
| ALK_3733 | ACGTTGGATGATGACAGGAAGAGCACAGTC | ACGTTGGATGGTGGCTGTCAGTATTTGGAG | GTATTTGGAGGAAAACCAC |
| ALK_3734 | ACGTTGGATGATGACAGGAAGAGCACAGTC | ACGTTGGATGGTGGCTGTCAGTATTTGGAG | cttTCAGTATTTGGAGGAAAACCACT |
| ALK_3735 | ACGTTGGATGGTGGCTGTCAGTATTTGGAG | ACGTTGGATGATGACAGGAAGAGCACAGTC | agcatTTTGACTCACCGGTGGAT |
| ALK_3749 | ACGTTGGATGACAGGTCAAGAGGCAGTTTTC | ACGTTGGATGCACTCATCTTCTAGGGATA | ctcCCTTTCTTCCAGAGACA |
| ALK_3824 | ACGTTGGATGTGAGGCAGTCTTTACTCACC | ACGTTGGATGTGGCCAAGATTGGAGACTTC | ttAGACTTCGGGATGGCCC |
| ALK_3832 | ACGTTGGATGGGGTGAGGCAGTCTTTACT | ACGTTGGATGTGGCCAAGATTGGAGACTTC | gctGGATGGCCGAGACATCT |
| BRAF_1390 | ACGTTGGATGTACTTACCATGCCACTTTCC | ACGTTGGATGGGCAGATTACAGTGGGACAA | ACAGTGGGACAAAGAATT |
| BRAF_1391 | ACGTTGGATGTACTTACCATGCCACTTTCC | ACGTTGGATGGGCAGATTACAGTGGGACAA | CAGTGGGACAAAGAATTG |
| BRAF_1399 | ACGTTGGATGTTACATACTTACCATGCCAC | ACGTTGGATGCAGATTACAGTGGGACAAAG | ACAAAGAATTGGATCTGGA |
| BRAF_1403 | ACGTTGGATGTTACATACTTACCATGCCAC | ACGTTGGATGCAGATTACAGTGGGACAAAG | ggCAAAGAATTGGATCTGGATCAT |
| BRAF_1406G | ACGTTGGATGTGGGCAGATTACAGTGGGAC | ACGTTGGATGACTTACCATGCCACTTTCCC | CACTTTCCCTTGACTACTGTT |
| BRAF_1455 | ACGTTGGATGGAAGGCTTGTAACTGCTGAG | ACGTTGGATGCCTTTTAGGTGATGTGGCAG | gggcTGTGGCAGTGAAAATGTT |
| BRAF_1460 | ACGTTGGATGGAAGGCTTGTAACTGCTGAG | ACGTTGGATGCCTTTTAGGTGATGTGGCAG | GCAGTGAAAATGTTGAATG |
| BRAF_1495 | ACGTTGGATGAATGTGACAGCACCTACACC | ACGTTGGATGAATTCACACAAGCTCACCTG | TGAGTACTCTACTTCATTTT |
| BRAF_1497 | ACGTTGGATGAATTCACACAAGCTCACCTG | ACGTTGGATGAATGTGACAGCACCTACACC | tccGCAGTTACAAGCCTTCAA |
| BRAF_1501 | ACGTTGGATGAATTCACACAAGCTCACCTG | ACGTTGGATGAATGTGACAGCACCTACACC | CAGTTACAAGCCTTCAAAAAT |
| BRAF_1502 | ACGTTGGATGAATGTGACAGCACCTACACC | ACGTTGGATGAATTCACACAAGCTCACCTG | CTCACCTGAGTACTCCTACT |
| BRAF_1738 | ACGTTGGATGACTTACACGCCAAGTCAATC | ACGTTGGATGCTTCGCAGACAAATTTTCAGG | AGACAAATTTTCAGGAAGGATACTAT |
| BRAF_1741 | ACGTTGGATGACTTACACGCCAAGTCAATC | ACGTTGGATGCTTCGCAGACAAATTTTCAGG | CAGACAAATTTTCAGGAAGGATAC |
| BRAF_1742 | ACGTTGGATGATGAGATCTACTGTTTTCC | ACGTTGGATGCCTATTTTTACTGTGAGGTC | acttTGAGGTCTTCATGAAGAAATATA |
| BRAF_1743 | ACGTTGGATGCCTATTTTTACTGTGAGGTC | ACGTTGGATGATGAGATCTACTGTTTTCC | TCCTTTACTTACTACACCTCAGA |

| | | | |
|---------------|---------------------------------|---------------------------------|------------------------------|
| BRAF_1781A_Rb | ACGTTGGATGTCTTCATGAAGACCTCACAG | ACGTTGGATGCCACTCCATCGAGATTTAC | CACTGTAGCTAGACCAAAA |
| BRAF_1783 | ACGTTGGATGACCCACTCCATCGAGATTTT | ACGTTGGATGTCTTCATGAAGACCTCACAG | CTCACAGTAAAAATAGGTGAT |
| BRAF_1784 | ACGTTGGATGACCCACTCCATCGAGATTTT | ACGTTGGATGTCTTCATGAAGACCTCACAG | TCACAGTAAAAATAGGTGATT |
| BRAF_1785 | ACGTTGGATGACCCACTCCATCGAGATTTT | ACGTTGGATGTCTTCATGAAGACCTCACAG | TCACAGTAAAAATAGGTGATTT |
| BRAF_1786 | ACGTTGGATGACCCACTCCATCGAGATTTT | ACGTTGGATGTCTTCATGAAGACCTCACAG | CACAGTAAAAATAGGTGATTTT |
| BRAF_1787 | ACGTTGGATGACCCACTCCATCGAGATTTT | ACGTTGGATGTCTTCATGAAGACCTCACAG | CTCACAGTAAAAATAGGTGATTTTG |
| BRAF_1798G | ACGTTGGATGATGGGACCCACTCCATCGAG | ACGTTGGATGTCTTCATGAAGACCTCACAG | GTGATTTTGGTCTAGCTACA |
| BRAF_1799T_F | ACGTTGGATGATGGGACCCACTCCATCGAG | ACGTTGGATGTCTTCATGAAGACCTCACAG | GGTGATTTTGGTCTAGCTACAG |
| BRAF_1799T_R | ACGTTGGATGATAGGTGATTTTGGTCTAGC | ACGTTGGATGATGGATCCAGACAACCTGTTT | CCCACTCCATCGAGATTTT |
| BRAF_721 | ACGTTGGATGCTGGAAAAGCAGCTTTTCGAC | ACGTTGGATGGTGATTTTTTACTTTGCAGG | cccgTTTTACTTTGCAGGTACGAAAA |
| BRAF_730 | ACGTTGGATGCTGGAAAAGCAGCTTTTCGAC | ACGTTGGATGCTTTGCAGGTACGAAAAACG | tgccGGTACGAAAAACGTTTTTTC |
| BRAF_736 | ACGTTGGATGCTGGAAAAGCAGCTTTTCGAC | ACGTTGGATGCTTTGCAGGTACGAAAAACG | ctGTACGAAAAACGTTTTTTCACCTTA |
| BRAF_769 | ACGTTGGATGGTACTACAACGCTGGTGA | ACGTTGGATGGTGACTTTTGTGCAAGCTG | GTCGAAAGCTGCTTTTTC |
| BRAF_770 | ACGTTGGATGGCATTGTGACTTTTGTGCG | ACGTTGGATGAACCACATGTTTGACAGCGG | TGTTTGACAGCGGAAACCC |
| BRAF_784 | ACGTTGGATGCAGTGGAACCTTCTGACTAC | ACGTTGGATGAGCTGCTTTTCCAGGGTTT | gatgTTCCAGGGTTTCCGCTGT |
| BRAF_785 | ACGTTGGATGAGCTGCTTTTCCAGGGTTT | ACGTTGGATGCAGTGGAACCTTCTGACTAC | GGTGAAATTTATAACCACATGTT |
| CDK4_70 | ACGTTGGATGAATTGGTGTGCGTGCCTATG | ACGTTGGATGACTCTTGAGGGCCACAAAGT | aGCCACTGTGGGGATCAC |
| CDK4_71 | ACGTTGGATGACTCTTGAGGGCCACAAAGT | ACGTTGGATGAATTGGTGTGCGTGCCTATG | GACAGTGTACAAGGCC |
| CTNNB1_101 | ACGTTGGATGTTACCACTCAGAGAAGGAGC | ACGTTGGATGACTGGCAGCAACAGTCTTAC | GTCTTACCTGGACTCTG |
| CTNNB1_109 | ACGTTGGATGCAGGATTGCCTTTACCACTC | ACGTTGGATGCAACAGTCTTACCTGGACTC | ctgACCTGGACTCTGGAATCCAT |
| CTNNB1_121 | ACGTTGGATGCAACAGTCTTACCTGGACTC | ACGTTGGATGCAGGATTGCCTTTACCACTC | CTCAGAGAAGGAGCTGTGG |
| CTNNB1_122 | ACGTTGGATGCAACAGTCTTACCTGGACTC | ACGTTGGATGCAGGATTGCCTTTACCACTC | ccaaTCAGAGAAGGAGCTGTG |
| CTNNB1_133 | ACGTTGGATGCATCCTCTTCCCTCAGGATTG | ACGTTGGATGCTCTGGAATCCATTCTGGTG | gcttGTGCCACTACCACAGCTCCT |
| CTNNB1_134 | ACGTTGGATGCTCTGGAATCCATTCTGGTG | ACGTTGGATGCATCCTCTTCCCTCAGGATTG | ttccgCAGGATTGCCTTTACCACTCAGA |
| CTNNB1_95 | ACGTTGGATGGACAGAAAAGCGGCTGTTAG | ACGTTGGATGGTGGTAGTGGCACCAGAATG | ACCAGAATGGATTCCAGAG |
| EGFR_2125G | ACGTTGGATGTTACCTTATACACCGTGCCG | ACGTTGGATGCCAACCAAGCTCTCTTGAGG | GCTCTCTTGAGGATCTTGAAG |
| EGFR_2126Aa | ACGTTGGATGTTACCTTATACACCGTGCCG | ACGTTGGATGCCAACCAAGCTCTCTTGAGG | cccctCTCTCTTGAGGATCTTGAAGG |
| EGFR_2155G | ACGTTGGATGCCTTATACACCGTGCCGAAC | ACGTTGGATGTCTCTTGAGGATCTTGAAGG | cgGAATTCAAAAAGATCAAAGTGCTG |
| EGFR_2156G_F | ACGTTGGATGCCTTATACACCGTGCCGAAC | ACGTTGGATGTCTCTTGAGGATCTTGAAGG | cAAAAGATCAAAGTGCTGG |
| EGFR_2156G_R | ACGTTGGATGGAGGATCTTGAAGGAAACTG | ACGTTGGATGCCTTACCTTATACACCGTGC | ACACCGTGCCGAACGCACCGGAG |
| EGFR_2281G | ACGTTGGATGAGGTTCCAGAGCCATGGACCC | ACGTTGGATGCAACATCTCCGAAAGCCAAC | AAAGCCAACAAGGAAATCCTC |
| EGFR_2303G | ACGTTGGATGCTCCAGGAAGCCTACGTGA | ACGTTGGATGACGGTGGAGGTGAGGCAGAT | gggAGGAAGCCTACGTGATGGCCA |
| EGFR_2303G | ACGTTGGATGCTCCAGGAAGCCTACGTGA | ACGTTGGATGTGTTCCCGACATAGTCCAG | CGTGGGGGTTGTCCACG |
| EGFR_2326C | ACGTTGGATGTCCAGGAAGCCTACGTGATG | ACGTTGGATGATGAGCTGCGTGATGAGCTG | GCAGATGCCAGCAGCG |

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| EGFR_2327G | ACGTTGGATGTCCAGGAAGCCTACGTGATG | ACGTTGGATGATGAGCTGCGTGATGAGCTG | TGGACAACCCCCACGTGTGCC |
| EGFR_2369C_F | ACGTTGGATGTGTTCCCGGACATAGTCCAG | ACGTTGGATGATCTGCCTCACCTCCACCGT | CCACCGTGCACTCATCA |
| EGFR_2369C_R | ACGTTGGATGATCTGCCTCACCTCCACCGT | ACGTTGGATGTGTTCCCGGACATAGTCCAG | ggggcGCCGAAGGGCATGAGCTGC |
| EGFR_2560A | ACGTTGGATGACGTACTGGTGA AACACCG | ACGTTGGATGTCTTTCTCTCCGCACCCAG | GGCCAGCCCAAATCTG |
| EGFR_2572C | ACGTTGGATGTCTTTCTCTCCGCACCCAG | ACGTTGGATGACGTACTGGTGA AACACCG | gggCAAGATCACAGATTTTGGG |
| EGFR_2573T_F | ACGTTGGATGTCTTTCTCTCCGCACCCAG | ACGTTGGATGACGTACTGGTGA AACACCG | ccTGTC AAGATCACAGATTTTGGGC |
| EGFR_2573T_R | ACGTTGGATGTCTTTCTCTCCGCACCCAG | ACGTTGGATGACGTACTGGTGA AACACCG | CTTCCGCACCCAGCAGTTTGGCC |
| EGFR_2582T | ACGTTGGATGTGGTATTCTTTCTCTCCGC | ACGTTGGATGAAACACCGCAGCATGTCAAG | TTTTGGGCTGGCCAAAC |
| ERBB2_2264T | ACGTTGGATGTGA AAATCCAGTGGCCATC | ACGTTGGATGGGGCTTACGTCTAAGATTTT | GGGATGTGTTTTCCCTC |
| ERBB2_2305G | ACGTTGGATGTCCTTCTGTCTCCTAGCA | ACGTTGGATGGAAAACACATCCCCAAAGC | CCCAAAGCCAACAAAGAAATCTTA |
| ERBB2_2329G | ACGTTGGATGAGAAGGCGGGAGACATATGG | ACGTTGGATGCTTGTCCCCAGGAAGCATA | AAGCATACGTGATGGCTGGT |
| FGFR2_1650 | ACGTTGGATGTTTCTCCTACTCACCATCC | ACGTTGGATGTGAAGATGATTGGGAAACAC | tgGGGAAACACAAGAATATCATAAA |
| FGFR2_755 | ACGTTGGATGTTCTTCCCTCTCTCCACCAG | ACGTTGGATGACTGTGGAGGCATTGCCG | gGGATGGGCCGGTGAGGC |
| FGFR3_1108 | ACGTTGGATGCTGAGGATGCCTGCATACAC | ACGTTGGATGCAACGCCCATGTCTTTGCAG | tggtCTGGTGGAGGCTGACGAGGCC |
| FGFR3_1118 | ACGTTGGATGAGCTGGTGGAGGCTGACGA | ACGTTGGATGAGGATGAACAGGAAGAAGCC | cctTAGCTGAGGATGCCTGCA |
| FGFR3_1948a | ACGTTGGATGGGACAACGTGATGAAGATCG | ACGTTGGATGAGGCGTCTACTGGCATGA | gggtGGCCGGGCTCACGTTGGTCGTCT |
| FGFR3_1948b | ACGTTGGATGACGTGCACAACCTGACTAC | ACGTTGGATGTACTGGCATGACCCCCACC | ccaAGGGCCGGGCTCACGTTGGTCGTCT |
| FGFR3_1949 | ACGTTGGATGGGACAACGTGATGAAGATCG | ACGTTGGATGAGGCGTCTACTGGCATGA | gggaaGGGCTCACGTTGGTCGTCT |
| FGFR3_2089 | ACGTTGGATGTCCTCAGCAGCTTGAAGAG | ACGTTGGATGTGCTCTGGGAGATCTTACG | GGGGCTCCCCGTACCCC |
| FGFR3_742 | ACGTTGGATGTGAGCGTCATCTGCCCCCA | ACGTTGGATGCAGCACCGCCGTCTGGTTG | GGGCCGGTGCGGGGAGC |
| FGFR3_746 | ACGTTGGATGAGCGTCATCTGCCCCACA | ACGTTGGATGCAGCACCGCCGTCTGGTTG | gacttCAGGATGGGCCGGTGCGGG |
| FLT3_2503 | ACGTTGGATGCATTGCCCTGACAACATAG | ACGTTGGATGGGGAAAGTGGTGAAGATATG | gGTGACTTTGATTGGCTCGA |
| GNAQ_626 | ACGTTGGATGACCTTGAGAATGGTCGATG | ACGTTGGATGCTCCACGAGAACTTGATCAT | cTTTTCTTCTCTGACCTT |
| GNAQ_627 | ACGTTGGATGTGCAGAATGGTCGATGTAGG | ACGTTGGATGCTGACTCCACGAGAACTTG | tATTTTCTTCTCTGACCT |
| HRAS_181C | ACGTTGGATGTGTTGGACATCCTGGATACC | ACGTTGGATGATGTACTGGTCCCGCATGG | tgtTCCCGCATGGCGCTGTACTCCTCT |
| HRAS_182A | ACGTTGGATGTGTTGGACATCCTGGATACC | ACGTTGGATGATGTACTGGTCCCGCATGG | acgccTGGCGCTGTACTCCTCC |
| HRAS_183G | ACGTTGGATGTGTTGGACATCCTGGATACC | ACGTTGGATGATGTACTGGTCCCGCATGG | CATGGCGCTGTACTCCTC |
| HRAS_35G | ACGTTGGATGGTTCTGGATCAGCTGGATGG | ACGTTGGATGCGATGACGGAATATAAGCTG | cGCTGGTGGTGGTGGGCGCCG |
| IDH1_394 | ACGTTGGATGAATATCCCCGGCTTGTGAG | ACGTTGGATGACATGACTTACTTGATCCCC | ggttATCCCATAAGCATGAC |
| IDH1_395a | ACGTTGGATGACATGACTTACTTGATCCCC | ACGTTGGATGAATATCCCCGGCTTGTGAG | gcTGGGTAAAACCTATCATCATAGGTC |
| IDH1_395b | ACGTTGGATGACATGACTTACTTGATCCCC | ACGTTGGATGAATATCCCCGGCTTGTGAG | cctGTA AACCTATCATCATAGGTC |
| IDH2_514 | ACGTTGGATGAAAACATCCCACGCCTAGTC | ACGTTGGATGTGGCCTACCTGGTCGCCAT | cctcCCTGGTCGCCATGGGCGTGCC |
| IDH2_515 | ACGTTGGATGTGGCCTACCTGGTCGCCAT | ACGTTGGATGAAAACATCCCACGCCTAGTC | AGCCCATCACCATTGGCA |
| JAK2_1849 | ACGTTGGATGGTTTTACTTACTCTCGTCTC | ACGTTGGATGTGATGAGCAAGCTTCTCAC | TGTTTTAAATATGGAGTATGT |

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| KIT_1676 | ACGTTGGATGCTGGGAACTCCCATTGTG | ACGTTGGATGTTTTCCCTTTCTCCCCACAG | ggggTGAAGTACAGTGGAAAGG |
| KIT_2446 | ACGTTGGATGAGCAGAGAATGGGTACTCAC | ACGTTGGATGCTTGGCAGCCAGAAATATCC | tttggGATTTTGGTCTAGCCAGA |
| KIT_2447 | ACGTTGGATGCTTGGCAGCCAGAAATATCC | ACGTTGGATGAGCAGAGAATGGGTACTCAC | ACATAATTAGAATCATTCTTGATG |
| KRAS_180T_F | ACGTTGGATGCATGTACTGGTCCCTCATTG | ACGTTGGATGTGGAGAAACCTGTCTCTTGG | CTTGGATATTCTCGACACAGCAGG |
| KRAS_181C | ACGTTGGATGCATGTACTGGTCCCTCATTG | ACGTTGGATGTGGAGAAACCTGTCTCTTGG | ggGGATATTCTCGACACAGCAGGT |
| KRAS_182A | ACGTTGGATGCATGTACTGGTCCCTCATTG | ACGTTGGATGTGGAGAAACCTGTCTCTTGG | GATATTCTCGACACAGCAGGTC |
| KRAS_183A | ACGTTGGATGTGGAGAAACCTGTCTCTTGG | ACGTTGGATGCATGTACTGGTCCCTCATTG | CATTGCACTGTACTCCTC |
| KRAS_34G_R | ACGTTGGATGAGGCCTGCTGAAAATGACTG | ACGTTGGATGCTGTATCGTCAAGGCACTC | ccaatGCACTCTTGCCTACGCCAC |
| KRAS_34T_35G_F | ACGTTGGATGCTGTATCGTCAAGGCACTC | ACGTTGGATGAGGCCTGCTGAAAATGACTG | TGGTAGTTGGAGCTT |
| KRAS_351A | ACGTTGGATGCTGAAGATGTACCTATGGTC | ACGTTGGATGTCCTGAGCCTGTTTTGTGTC | TTCTAGAAGGCAAATCACA |
| KRAS_35G_F | ACGTTGGATGCTGTATCGTCAAGGCACTC | ACGTTGGATGAGGCCTGCTGAAAATGACTG | TTGTGGTAGTTGGAGCTG |
| KRAS_35T_34G_R | ACGTTGGATGCTGTATCGTCAAGGCACTC | ACGTTGGATGAGGCCTGCTGAAAATGACTG | ACTCTGCCTACGCCAA |
| KRAS_37G_F | ACGTTGGATGCTGTATCGTCAAGGCACTC | ACGTTGGATGAGGCCTGCTGAAAATGACTG | TGGTAGTTGGAGCTGGT |
| KRAS_38G_F | ACGTTGGATGCTGTATCGTCAAGGCACTC | ACGTTGGATGAGGCCTGCTGAAAATGACTG | CTTGTGGTAGTTGGAGCTGGTG |
| KRAS_436G | ACGTTGGATGCAGTGTTACTTACCTGTCTTG | ACGTTGGATGGCTCAGGACTTAGCAAGAAG | ttGAATTCCTTTTATTGAAACATCA |
| KRAS_437C | ACGTTGGATGGCTCAGGACTTAGCAAGAAG | ACGTTGGATGTTCAAGTGTACTTACCTGTC | acGTTACTTACCTGTCTTGTCTTT |
| MAP2K1_167A | ACGTTGGATGAAAGCGCCTTGAGGCCTTTC | ACGTTGGATGTCTCAAAGTCGTATCCTTC | CTCCACCTTCTGCTTC |
| MAP2K1_171G | ACGTTGGATGTTGATGAGCAGCAGCGAAAG | ACGTTGGATGAAGTCGTCATCCTTCAGTTC | AGTTCTCCACCTTCTG |
| MAP2K1_199G | ACGTTGGATGTGAACACCACACCGCCATTG | ACGTTGGATGAGAAGGTGGGAGAACTGAAG | GGAGAACTGAAGGATGAC |
| MET_3743 | ACGTTGGATGGTTGCTGATTTTGGTCTTGC | ACGTTGGATGGCAGCTTTCACCTGTTTTG | GTGTACACTATAGTATTCTTTATCA |
| MET_3757 | ACGTTGGATGGCAGCTTTCACCTGTTTTG | ACGTTGGATGGTTGCTGATTTTGGTCTTGC | GCCAGAGACATGTATGATAAAGAATAC |
| MET_3803 | ACGTTGGATGCATCTGACTTGGTGGTAAAC | ACGTTGGATGAAAACAGGTGCAAAGCTGCC | agtgGCAAAGCTGCCAGTGAAGTGA |
| NOTCH1_4724 | ACGTTGGATGAGCTGTTGCGCAGCTGCTC | ACGTTGGATGAGCATGTACCCGAGAGGCTG | GCTGGCGGCCGGCACGC |
| NOTCH1_4757 | ACGTTGGATGAGCTCCCGCAGGAAGTGAA | ACGTTGGATGGTGGTGGTGGTCTGATGC | agtCTGATGCCGCCGGAGCAGC |
| NOTCH1_4781 | ACGTTGGATGCACGCTTGAAGACCACGTTG | ACGTTGGATGAGCTGCGCAACAGCTCCTTC | tgCAGCTCCTTCCACTTCC |
| NOTCH1_4796 | ACGTTGGATGCACGCTTGAAGACCACGTTG | ACGTTGGATGACAGCTCCTTCCACTTCTG | gggttACTTCTGCGGGAGCTCAGCC |
| NOTCH1_4802 | ACGTTGGATGCACGCTTGAAGACCACGTTG | ACGTTGGATGACAGCTCCTTCCACTTCTG | ggggCTGCGGGAGCTCAGCCCGTGC |
| NOTCH1_5036 | ACGTTGGATGTCTGGAAGCACTGCGAGGAG | ACGTTGGATGATTGTCCGCCAGCTCCAT | CAGCTCCATCGTCTACC |
| NOTCH1_7378 | ACGTTGGATGCTGGCGGTGCACACTATTC | ACGTTGGATGACCAGCGAGGATGGCAGCGA | ccGGGCAGGGCGGGGCTCTCCT |
| NRAS_181C | ACGTTGGATGTGTCCTCATGTATTGGTCTC | ACGTTGGATGGTGAACCTGTTTGTGGAC | TACTGGATACAGCTGGA |
| NRAS_181C | ACGTTGGATGTGTCCTCATGTATTGGTCTC | ACGTTGGATGGTGAACCTGTTTGTGGAC | ACATACTGGATACAGCTGGA |
| NRAS_182A | ACGTTGGATGGTGAACCTGTTTGTGGAC | ACGTTGGATGTGTCCTCATGTATTGGTCTC | ctcgCATGGCACTGTACTCTTCT |
| NRAS_182A | ACGTTGGATGTGTCCTCATGTATTGGTCTC | ACGTTGGATGGTGAACCTGTTTGTGGAC | aTCATGGCACTGTACTCTTCT |
| NRAS_183A | ACGTTGGATGGTGAACCTGTTTGTGGAC | ACGTTGGATGTGTCCTCATGTATTGGTCTC | CATGGCACTGTACTCTTCT |

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| NRAS_183A | ACGTTGGATGGTCAAACCTGTTTGTGGAC | ACGTTGGATGTGTCCTCATGTATTGGTCTC | ttgtTCTCTCATGGCACTGTACTCTTC |
| NRAS_34G | ACGTTGGATGAGTGGTTCTGGATTAGCTGG | ACGTTGGATGGACTGAGTACAAACTGGTGG | caaaTGGTGGTGGTTGGAGCA |
| NRAS_34G | ACGTTGGATGGACTGAGTACAAACTGGTGG | ACGTTGGATGAGTGGTTCTGGATTAGCTGG | tggCAGTGCCTTTTTCCAACACCAC |
| NRAS_35G | ACGTTGGATGAGTGGTTCTGGATTAGCTGG | ACGTTGGATGGACTGAGTACAAACTGGTGG | GGTGGTGGTTGGAGCAG |
| NRAS_35G | ACGTTGGATGGACTGAGTACAAACTGGTGG | ACGTTGGATGAGTGGTTCTGGATTAGCTGG | GGTGGTGGTTGGAGCAG |
| NRAS_37G | ACGTTGGATGAGTGGTTCTGGATTAGCTGG | ACGTTGGATGGACTGAGTACAAACTGGTGG | TGGTGGTTGGAGCAGGT |
| NRAS_37G | ACGTTGGATGAGTGGTTCTGGATTAGCTGG | ACGTTGGATGGACTGAGTACAAACTGGTGG | TGGTGGTTGGAGCAGGT |
| NRAS_38G | ACGTTGGATGAGTGGTTCTGGATTAGCTGG | ACGTTGGATGGACTGAGTACAAACTGGTGG | GGTGGTTGGAGCAGGTG |
| NRAS_38G | ACGTTGGATGAGTGGTTCTGGATTAGCTGG | ACGTTGGATGGACTGAGTACAAACTGGTGG | agaggTTCAGTGCCTTTTTCCAACA |
| PDGFRA_1682 | ACGTTGGATGATGTCCATCTGGGCTGATTG | ACGTTGGATGCCTGTCCTGGTCATTTATAG | TGAAATTCGCTGGAGGG |
| PDGFRA_2525 | ACGTTGGATGAGATCTGTGACTTTGGCCTG | ACGTTGGATGAAGTGAGGACGTACTGCC | gggcGTTCGAATCATGCATGATG |
| PIK3CA_1035T | ACGTTGGATGGCATCAGCATTGACTTTACC | ACGTTGGATGAAAAATTTCTTGCAACC | TTTGTCAACCTACGTGAA |
| PIK3CA_1258T | ACGTTGGATGGTTTTATAATTTAGACTAGTG | ACGTTGGATGAGTTTATATTTCCCATGCC | TTTCCCATGCCAATGGAC |
| PIK3CA_1624G | ACGTTGGATGTAGCACTTACCTGTGACTCC | ACGTTGGATGGCAATTTCTACACGAGATCC | TTTCTACACGAGATCCTCTCTCT |
| PIK3CA_1633G | ACGTTGGATGTACACGAGATCCTCTCTCTG | ACGTTGGATGTAGCACTTACCTGTGACTCC | ATAGAAAATCTTTCTCTGCT |
| PIK3CA_1634A | ACGTTGGATGTAGCACTTACCTGTGACTCC | ACGTTGGATGGCAATTTCTACACGAGATCC | CCTCTCTCTGAAATCACTG |
| PIK3CA_1635G | ACGTTGGATGTAGCACTTACCTGTGACTCC | ACGTTGGATGGCAATTTCTACACGAGATCC | cTCCTCTCTGAAATCACTGA |
| PIK3CA_263G | ACGTTGGATGTAACAAGAAGCAGAAAGGG | ACGTTGGATGGGTTGAAAAAGCCGAAGGTC | gTGAAAAAGCCGAAGGTCACAAAGT |
| PIK3CA_3129G | ACGTTGGATGAACTGAGCAAGAGGCTTTGG | ACGTTGGATGTCCATTTTTGTTGTCCAGCC | aACCATGATGTGCATCATT |
| PIK3CA_3139C | ACGTTGGATGAACTGAGCAAGAGGCTTTGG | ACGTTGGATGTCCATTTTTGTTGTCCAGCC | cTTGTCCAGCCACCATGAT |
| PIK3CA_3140A | ACGTTGGATGTCCATTTTTGTTGTCCAGCC | ACGTTGGATGAACTGAGCAAGAGGCTTTGG | TCATGAAACAATGAATGATGCAC |
| PIK3R1_1678 | ACGTTGGATGTTTCTCAGCTGGATAAGGTC | ACGTTGGATGAAGCAGGCAGCTGAGTATCG | CAGCTGAGTATCGAGAAATT |
| PIK3R1_1692 | ACGTTGGATGAAGCAGGCAGCTGAGTATCG | ACGTTGGATGTTTCTCAGCTGGATAAGGTC | TAAGGTCTGGTTAATGCT |
| PTPN11_179 | ACGTTGGATGTTCTCCCCTCCATACAGGTC | ACGTTGGATGAAGAAATGGAGCTGTCACCC | acaCACATCAAGATTCAGAACACTG |
| PTPN11_181 | ACGTTGGATGTTCTCCCCTCCATACAGGTC | ACGTTGGATGATGGAGCTGTCACCCACATC | AGATTCAGAACACTGGT |
| PTPN11_182 | ACGTTGGATGAAGAAATGGAGCTGTCACCC | ACGTTGGATGTTCTCCCCTCCATACAGGTC | CCCCTCCATACAGGTCATAGTAA |
| PTPN11_214 | ACGTTGGATGTGCCCGTGATGTTCCATGTA | ACGTTGGATGACTATGACCTGTATGGAGGG | tggATGGAGGGGAGAAATTT |
| PTPN11_226 | ACGTTGGATGTGCCCGTGATGTTCCATGTA | ACGTTGGATGACTATGACCTGTATGGAGGG | ggggtGGAGAAATTTGCCACTTTGGCT |
| PTPN11_227 | ACGTTGGATGACTATGACCTGTATGGAGGG | ACGTTGGATGTTAATTGCCCGTGATGTTCC | TTCCATGTAATACTGGACCAAC |
| PTPN11_455 | ACGTTGGATGTTGCTCTCCCCTTTGTCATC | ACGTTGGATGTTCTGTACGAGAGAGCCAG | atgtAGATTTTGTCTTTCTGTGC |
| RET_2753 | ACGTTGGATGCATCACTTTGCGTGGTGTAG | ACGTTGGATGTCTTTAGGGTCGGATTCCAG | tgAGGGTCGGATTCCAGTTAAATGGA |
| SMO_1604 | ACGTTGGATGACCAGGTACGCCTCCAGATG | ACGTTGGATGCATGTTTGAAGTGGCATCG | TGGCATCGCCATGAGCACCT |
| SMO_1918 | ACGTTGGATGCCATACTGCCCCAGGATATT | ACGTTGGATGCTTCTCCAGAAGCTTGAAC | ggtcCCTGGAGTTGCCACAGGGG |
| SMO_595 | ACGTTGGATGAGTTCAACAGTTCAGGCCAG | ACGTTGGATGACGTCCTCGTACCAGCTCTT | CTTGGGGTTGTCTGTCC |

Supplemental Table 4. Primers used for amplification of FGFR4 and CTNNB1 exons.

| gene | Forward Primer ID | Forward Primer Sequence | Reverse Primer ID | Reverse Primer Sequence |
|--------|--|--------------------------|--|---------------------------|
| CTNNB1 | CTNNB1_153648_L_6262139_chr3_41240936_FFPE | CAATGGGTCATATCACAGATTCTT | CTNNB1_153648_R_6262140_chr3_41241286_FFPE | TGACTTTCAGTAAGGCAATGAAAA |
| CTNNB1 | CTNNB1_153649_L_6262169_chr3_41241108_FFPE | GAATCCATTCTGGTGCCACT | CTNNB1_153649_R_6262170_chr3_41241353_FFPE | TTTTCTTCACCACAACATTTTATTT |
| CTNNB1 | CTNNB1_91709_L_9805086_chr3_41240700_20 | TCACTGAGCTAACCCCTGGCT | CTNNB1_91709_R_9805087_chr3_41241779_21 | TCCACAGTTCAGCATTACCT |
| FGFR4 | FGFR4_130022_L_8823624_chr5_176448806_20 | GGCCTTAGGCTCTGGCTACT | FGFR4_130022_R_8823625_chr5_176449583_20 | ATCCTTCCAGCTTTGCTCA |
| FGFR4 | FGFR4_130025_L_9694020_chr5_176449714_20 | TGTGTGGGTGTCAAGGAGTG | FGFR4_130025_R_9694021_chr5_176450703_20 | TGCTGGAGGTCAAGGAGTCT |
| FGFR4 | FGFR4_130030_L_9783666_chr5_176450189_20 | TCTAGCAGGGAGTGAAGGGA | FGFR4_130030_R_9783667_chr5_176451368_20 | TAGCAGAAGGGGAACAGAG |
| FGFR4 | FGFR4_130033_L_10235316_chr5_176451117_20 | GTGGGCAGGATGAGGATCTA | FGFR4_130033_R_10235317_chr5_176451808_20 | CCACACTAACCCCTGTGCTT |
| FGFR4 | FGFR4_130038_L_10561130_chr5_176451659_20 | AGCAGGGTAAGCAGGAGACA | FGFR4_130038_R_10561131_chr5_176452606_20 | GGACTCCACCTCTGAGCTA |
| FGFR4 | FGFR4_130041_L_11389048_chr5_176451936_20 | TTTCCCCTATGTGCAAGTCC | FGFR4_130041_R_11389049_chr5_176452685_20 | CACAGGCCAACAGAGACTGA |
| FGFR4 | FGFR4_130042_L_8941514_chr5_176452456_20 | CCTGGGACTGGCATAACTA | FGFR4_130042_R_8941515_chr5_176453745_20 | CAGCCTGGAGATGGAGAAAG |
| FGFR4 | FGFR4_130045_L_11650826_chr5_176452893_20 | GCAGTTCTCCCTGGAGTCAG | FGFR4_130045_R_11650827_chr5_176453364_20 | CAGCCTGGAGATGGAGAAAG |
| FGFR4 | FGFR4_130046_L_15490357_chr5_176452928_ | tgcaccactatgggagttc | FGFR4_130046_R_15490358_chr5_176453254_ | tcgaaattctggattcaagc |
| FGFR4 | FGFR4_130051_L_10369746_chr5_176454680_20 | CAGCCTAGCAAGGATTACAGC | FGFR4_130051_R_10369747_chr5_176455355_20 | GCACTCCACGATCACGTACA |
| FGFR4 | FGFR4_130053_L_11492036_chr5_176454891_20 | TCATCAACTGCTTGGTGTC | FGFR4_130053_R_11492037_chr5_176455648_20 | GGAGAAGTCGGGACATTGAA |
| FGFR4 | FGFR4_130056_L_10978760_chr5_176455453_20 | TCTGTAAAGTGGGTGGAGGG | FGFR4_130056_R_10978761_chr5_176456192_20 | GTACACCCGGTCAAACAAGG |
| FGFR4 | FGFR4_130060_L_10307596_chr5_176455495_20 | GTGCTGGTGACTGAGGACAA | FGFR4_130060_R_10307597_chr5_176456220_20 | CCCAGACCAAATCTGAAGGA |
| FGFR4 | FGFR4_130061_L_10657860_chr5_176455906_20 | CCTTCAGATTGGTCTGGGA | FGFR4_130061_R_10657861_chr5_176456705_20 | AAGAGGAGGAGGAGGACGAG |
| FGFR4 | FGFR4_130066_L_10017316_chr5_176456694_20 | TCAAACCTCCCACTCAAGCA | FGFR4_130066_R_10017317_chr5_176457397_20 | AATAGGGTCCGAAGGTCAGG |
| FGFR4 | FGFR4_130069_L_10799800_chr5_176456745_20 | CAGAGGCTACCTTCAAGCA | FGFR4_130069_R_10799801_chr5_176457994_20 | GAACCTCTGCTGGTATTGG |
| FGFR4 | FGFR4_214602_L_7486413_chr5_176449091_FFPE | aaaataagggaagAGCCCC | FGFR4_214602_R_7486414_chr5_176449390_FFPE | ATCCTTCCAGCTTTGCTCA |
| FGFR4 | FGFR4_214609_L_7486453_chr5_176449917_FFPE | TGTGCGGTGTGTTCTTTGTA | FGFR4_214609_R_7486454_chr5_176450249_FFPE | AGGTGAGATTCTGCAGGACG |
| FGFR4 | FGFR4_214610_L_7486473_chr5_176450093_FFPE | GTGGCCACTGGTACAAGGA | FGFR4_214610_R_7486474_chr5_176450344_FFPE | GGGACAGAGGAAGCATCTA |
| FGFR4 | FGFR4_214620_L_7486513_chr5_176450272_FFPE | TAGCAGGGAGTGAAGGGATG | FGFR4_214620_R_7486514_chr5_176450592_FFPE | TGCATGCAGTTTCTCTCCA |
| FGFR4 | FGFR4_214621_L_7486579_chr5_176450424_FFPE | CCCAGCAAGGTCAGTAGGTC | FGFR4_214621_R_7486580_chr5_176450771_FFPE | GGGGACTGATGAAGGAATGA |
| FGFR4 | FGFR4_214622_L_7486619_chr5_176450601_FFPE | GGGAACACCGTCAAGTTCC | FGFR4_214622_R_7486620_chr5_176450786_FFPE | TGCTTGTAGGTATGAGGGGAC |
| FGFR4 | FGFR4_214625_L_7486633_chr5_176451217_FFPE | GGATCTAGCCTCTGGTCTCT | FGFR4_214625_R_7486634_chr5_176451515_FFPE | CATCTGAGTCCATCCTGCCT |
| FGFR4 | FGFR4_214630_L_7486683_chr5_176451841_FFPE | TTGAACTTGAGGAAGGCTGG | FGFR4_214630_R_7486684_chr5_176452172_FFPE | ACCAAGGTGGGAGAAGAAT |
| FGFR4 | FGFR4_214631_L_7486703_chr5_176452002_FFPE | GAGCTGCTGTGCAAGGTGTA | FGFR4_214631_R_7486704_chr5_176452197_FFPE | AACAGGGAAGCTGGGGAG |
| FGFR4 | FGFR4_214634_L_7486723_chr5_176452152_FFPE | ATTCTTCTCCACCTTGGGT | FGFR4_214634_R_7486724_chr5_176452485_FFPE | GGCCAACAGAGACTGACCAC |
| FGFR4 | FGFR4_214638_L_7486763_chr5_176452659_FFPE | GGGAGGGACTGAGTTAGGGT | FGFR4_214638_R_7486764_chr5_176453001_FFPE | AGACTTGGTTCTGCCTGCTG |
| FGFR4 | FGFR4_214639_L_7486773_chr5_176452824_FFPE | CTTGCTGTGCTCCTGCT | FGFR4_214639_R_7486774_chr5_176453150_FFPE | GGGAACTCCATAGTGGGTC |
| FGFR4 | FGFR4_214640_L_7486793_chr5_176452999_FFPE | CTCCACTTTCAGTTCTCC | FGFR4_214640_R_7486794_chr5_176453253_FFPE | GGAGAAAGTCCAGCCTCAGA |

| | | | | |
|-------|--|-----------------------|--|----------------------|
| FGFR4 | FGFR4_214643_L_chr5_176453157_FFPE | aggtgctgctgagctgtgt | FGFR4_214643_R_chr5_176453385_FFPE | cacctttgagcatcttgacg |
| FGFR4 | FGFR4_214646_L_7486813_chr5_176454873_FFPE | gcctctGCATGCTCCCT | FGFR4_214646_R_7486814_chr5_176455118_FFPE | GTGGAGAGGCTGCCAAAG |
| FGFR4 | FGFR4_214651_L_7486853_chr5_176455076_FFPE | GGCCGTTAGGGTG CAGA | FGFR4_214651_R_7486854_chr5_176455369_FFPE | GAGAGACTGAGAGGGGCTCA |
| FGFR4 | FGFR4_214652_L_7486893_chr5_176455238_FFPE | CCTCGGAGCAGTGAGGG | FGFR4_214652_R_7486894_chr5_176455414_FFPE | GGAGAAGTCGGGACATTGAA |
| FGFR4 | FGFR4_214655_L_7486913_chr5_176455558_FFPE | tctgtaaagtggtGGAGGG | FGFR4_214655_R_7486914_chr5_176455868_FFPE | AGAGTCCCACAGGTCCTCG |
| FGFR4 | FGFR4_214658_L_7486943_chr5_176455793_FFPE | GAGATGGGGCAGAACTGGAT | FGFR4_214658_R_7486944_chr5_176456070_FFPE | CAAATCTGAAGGAGCCCTCG |
| FGFR4 | FGFR4_214661_L_7486959_chr5_176456117_FFPE | ACAGCTGTGGTGGGTCATGT | FGFR4_214661_R_7486960_chr5_176456448_FFPE | TAGTGTGTCTCTTGCCG |
| FGFR4 | FGFR4_214664_L_7487013_chr5_176456794_FFPE | CATCAAAC TCCCCACCAAAC | FGFR4_214664_R_7487014_chr5_176457071_FFPE | CGGTCAGGCCAGATGAG |
| FGFR4 | FGFR4_214673_L_7487039_chr5_176457032_FFPE | CTCTGCCTGCTCCCTC | FGFR4_214673_R_7487040_chr5_176457379_FFPE | CCCATGCTATCAAGGTCGAG |

Supplemental Table 5. Primers used in Sanger Sequencing of all identified mutations.

| Mutation ID | Forward Primer | Reverse Primer |
|--------------------|---|--|
| BRAF_1783 | tgtaaacgacggccagtTGCTTGCTCTGATAGGAAAATG | caggaaacagctatgaccTCAGGGCCAAAAATTTAATCAG |
| BRAF_1799 | tgtaaacgacggccagtTGCTTGCTCTGATAGGAAAATG | caggaaacagctatgaccTCAGGGCCAAAAATTTAATCAG |
| CTNNB1_121 | TTTGATGGAGTTGGACATGG | GGCAATGAAAAATAATACTCTTACCA |
| CTNNB1_134 | TTTGATGGAGTTGGACATGG | GGCAATGAAAAATAATACTCTTACCA |
| FGFR4_1648 | GTTAGGGTGCAGAGCCAAAG | CGGGACTCCAGATACTGCAT |
| HRAS_181 | AGAGGCTGGCTGTGTGAACT | TCACGGGGTTCACCTGTACT |
| HRAS_183 | AGAGGCTGGCTGTGTGAACT | TCACGGGGTTCACCTGTACT |
| KRAS_35 | GTGTGACATGTTCTAATATAGTCA | CTGTATCAAAGAATGGTCCTGCAC |
| KRAS_38 | GTGTGACATGTTCTAATATAGTCA | CTGTATCAAAGAATGGTCCTGCAC |
| MAP2K1_171 | tgtaaacgacggccagtGGAACAGGACCAACTTGGAG | caggaaacagctatgaccGcTTGTGGGAGACCTTGAAC |
| NRAS_181 | CCCCTTACCCTCCACACC | CACAAAGATCATCCTTTCAGAGAA |
| NRAS_183 | CCCCTTACCCTCCACACC | CACAAAGATCATCCTTTCAGAGAA |
| PIK3CA_1624 | TTGAAAATGTATTTGCTTTTTCTGT | ACATGCTGAGATCAGCCAAA |
| PIK3CA_1633 | TTGAAAATGTATTTGCTTTTTCTGT | ACATGCTGAGATCAGCCAAA |
| PIK3CA_3140 | tgtaaacgacggccagtCTCAATGATGCTTGGCTCTG | caggaaacagctatgaccTGGAATCCAGAGTGAGCTTTC |
| PTPN11_226 | CCTTGCCTCCCTTCCAAT | TCTGACACTCAGGGCACAAG |

Supplemental Table 6. Clinical characteristics of tumor samples with identified mutations.

| Sample ID | Tumor | Mutation | Age at Diagnosis | Sex | Primary Site | Stage | Outcome |
|-----------|-------|--|------------------|-----|-----------------------|-------------------------|---------|
| R71 | ARMS | KRAS_38G>A (G13D) | 3 | F | Gluteal | 3 (Group III) | DOD |
| R1 | ERMS | PIK3CA_1624G>A (E542K) | 14 | F | Infratemporal Fossa | 3 (Group III) | DOD |
| R6 | ERMS | FGFR4_1648G>C (V550L) | 5 | M | Paratesticular | 1 (Group I) | Alive |
| R7 | ERMS | CTNNB1_134C>A (S45Y) | 3 | F | Perineum | 2 (Group II) | Alive |
| R11 | ERMS | CTNNB1_121A>G (T41A), NRAS_181C>A (Q61K) | 10 months | M | Pelvis | 4 | Alive |
| R13 | ERMS | FGFR4_1648G>C (V550L) | 21 | F | Chest Wall | 4 | DOD |
| R29 | ERMS | NRAS_181C>A (Q61K) | 18 | M | Anterior Mediastinum | 4 | Alive |
| R31 | ERMS | FGFR4_1648G>C (V550L) | | | Cell line | | |
| R33 | ERMS | PTPN11_226G>C (E76Q) | 3 | M | Bladder | 3 (Group III) | |
| R35 | ERMS | NRAS_183A>T (Q61H) | | | Cell line | | |
| R36 | ERMS | FGFR4_1648G>C (V550L) | 11 | M | Neck | 4 | DOD |
| R43 | ERMS | PIK3CA_1633G>A (E545K) | 13 | F | Hemi-diaphragm | 3 (Group III) | DOD |
| R44 | ERMS | NRAS_181C>A (Q61K) | 17 | M | Pelvis | 4 | DOD |
| R48 | ERMS | PIK3CA_3140A>G (H1047R) | 37 | M | Pterygopalatine Fossa | 3 (Group III) | DOD |
| R50 | ERMS | KRAS_35G>A (G12D) | 1 | M | Pelvis | 4 | DOD |
| R51 | ERMS | HRAS_181C>A (Q61K) | | | Cell line | | |
| R60 | ERMS | BRAF_1799T>A (V600E) | 27 | M | Femur | information unavailable | DOD |
| R61 | ERMS | KRAS_34G>T (G12C) | 2 | M | Retroperitoneum | 3 (Group III) | DOD |
| ES2 | ES | BRAF_1799T>A (V600E) | | | Cell line | | |
| ES9 | ES | CTNNB1_133_135delTCT (S45del) | 14 | M | Pelvis | 4 | DOD |
| ES17 | ES | NRAS_181C>A (Q61K) | 32 | M | Scapula | 4 | DOD |
| NB2 | NB | ALK_3824G>A (R1275Q) | 2 | M | Adrenal | 4 | DOD |
| NB3 | NB | ALK_3522C>A (F1174L) | 1 | M | Adrenal | 4 | DOD |
| NB10 | NB | ALK_3520T>C (F1174L) | 11 | F | Posterior mediastinum | 4 | Alive |
| NB12 | NB | ALK_3733T>G (F1245V) | 3 | M | Adrenal | 3 | Alive |
| NB23 | NB | KRAS_35G>T (G12V) | 3 | M | Adrenal | 4 | DOD |
| NB30 | NB | ALK_3522C>A (F1174L) | 5 | M | Adrenal | 4 | DOD |
| NB32 | NB | BRAF_1783T>C (F595L) | 14 | M | Adrenal | 4 | DOD |
| NB39 | NB | ALK_3522C>A (F1174L) | 5 | F | Adrenal | 4 | DOD |
| NB44 | NB | ALK_3824G>A (R1275Q) | 4 | M | Adrenal | 4 | DOD |
| NB54 | NB | ALK_3522C>A (F1174L) | 1 | M | Adrenal | 4 | DOD |
| NB58 | NB | ALK_3521T>G (F1174C) | 6 | F | Adrenal | 4 | DOD |

| | | | | | | | |
|-------|----|----------------------|-----------|---|-----------------------|---|-------|
| NB62 | NB | ALK_3734T>G (F1245C) | 29 | F | Retroperitoneal | 4 | DOD |
| NB81 | NB | ALK_3520T>C (F1174L) | 19 | F | Adrenal | 4 | DOD |
| NB83 | NB | ALK_3520T>C (F1174L) | 6 | F | Adrenal | 1 | Alive |
| NB109 | NB | ALK_3824G>A (R1275Q) | 1 | F | Paraspinal | 2 | Alive |
| NB129 | NB | ALK_3824G>A (R1275Q) | 4 | M | Posterior mediastinum | 4 | DOD |
| NB134 | NB | ALK_3824G>A (R1275Q) | 6 weeks | M | Adrenal | 3 | Alive |
| NB135 | NB | ALK_3824G>A (R1275Q) | 1 | M | Adrenal | 4 | Alive |
| NB139 | NB | MAP2K1_171G>T (K57N) | 2 | F | Pre-sacral | 3 | Alive |
| NB151 | NB | NRAS_181C>A (Q61K) | 6 | M | Adrenal | 4 | DOD |
| NB158 | NB | BRAF_1799T>A (V600E) | 11 months | M | Adrenal | 3 | Alive |
| NB171 | NB | ALK_3824G>A (R1275Q) | 8 | F | Adrenal | 4 | Alive |
| NB174 | NB | ALK_3522C>A (F1174L) | 2 | M | Adrenal | 4 | DOD |
| NB188 | NB | ALK_3522C>A (F1174L) | 5 | M | Adrenal | 4 | DOD |
| NB191 | NB | ALK_3522C>A (F1174L) | 2 | M | Adrenal | 4 | DOD |